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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/765,272	01/22/2001	Gil H. Choi	PB340P2C2	9690

22195 7590 05/06/2003

HUMAN GENOME SCIENCES INC
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EXAMINER

DUFFY, PATRICIA ANN

ART UNIT PAPER NUMBER

1645

DATE MAILED: 05/06/2003

VB

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

01/765,272

Applicant(s)

Chai et al

Examiner

Duffy

Group Art Unit

1645

—The MAILING DATE of this communication appears on the cover sheet beneath the correspondence address—

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE three MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, such period shall, by default, expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).

Status

- ☒ Responsive to communication(s) filed on 10-7-02 + 2-14-03
- ☐ This action is **FINAL**.
- ☐ Since this application is in condition for allowance except for formal matters, **prosecution as to the merits is closed** in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 1 1; 453 O.G. 213.

Disposition of Claims

- ☒ Claim(s) 10-12, 14-92 is/are pending in the application.
Of the above claim(s) 10-12, 14-21, 33, 48, 61 + 73 is/are withdrawn from consideration.
- ☐ Claim(s) _____ is/are allowed.
- ☒ Claim(s) 22-32, 34-47, 49-60, 62-72 + 74-92 is/are rejected.
- ☐ Claim(s) _____ is/are objected to.
- ☒ Claim(s) 10-12, 14-92 are subject to restriction or election requirement.

Application Papers

- ☐ See the attached Notice of Draftsperson's Patent Drawing Review, PTO-948.
- ☐ The proposed drawing correction, filed on _____ is ☐ approved ☐ disapproved.
- ☐ The drawing(s) filed on _____ is/are objected to by the Examiner.
- ☐ The specification is objected to by the Examiner.
- ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. § 119 (a)-(d)

- ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d).
 - ☐ All ☐ Some* ☐ None of the CERTIFIED copies of the priority documents have been received.
 - ☐ received in Application No. (Series Code/Serial Number) _____.
 - ☐ received in this national stage application from the International Bureau (PCT Rule 1 7.2(a)).

*Certified copies not received: _____

Attachment(s)

- ☒ Information Disclosure Statement(s), PTO-1449, Paper No(s). 12
- ☒ Notice of Reference(s) Cited, PTO-892
- ☐ Notice of Draftsperson's Patent Drawing Review, PTO-948
- ☐ Interview Summary, PTO-413
- ☐ Notice of Informal Patent Application, PTO-152
- ☐ Other _____

Office Action Summary

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DETAILED ACTION

1. The responses filed October 7, 2002 and February 14, 2003 has been entered into the record. Pursuant to the amendment of February 14, 2003, claims 10-12, 14-92 are pending.

Specification

2. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

Election/Restriction

3. Applicant's election with traverse of Group 1, SEQ ID NOS:65 and 66 in Paper No. 9 is acknowledged. The traversal is on the ground(s) that the members of the Markush group are sufficiently few in number or so closely related that a search and examination of all the claims of the entire application can be made without serious burden and that even though patentably distinct inventions appear in a single application, restriction remains improper unless the examiner can show that the search and examination of these groups would entail a "serious burden". Applicant's arguments have been fully considered but are not found to be fully persuasive.

This is not found persuasive because the term "distinct" is defined to mean that two or more subjects as disclosed are related, for example, as product and method of use, etc., but are capable of separate manufacture, use or sale as claimed, and are patentable over each other (see MPEP 802.01). In the instant situation, the inventions of Groups I-VI and all Markush members are drawn to distinct inventions which are related as separate

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products capable of separate manufacture, use or sale as described in the previous Office Action. Restrictions between the inventions is deemed to be proper for the reasons previously set forth. In regard to burden of search and examination, MPEP 803 states that a burden can be shown if the examiner shows either separate classification, different field of search or separate status in the art. In the instant case a burden has been established in showing that the inventions of Groups I-VI are classified separately necessitating different searches of issued U.S. Patents. However, classification of subject matter is merely one indication of the burdensome nature of search. The literature search, particularly relevant in this art, is not co-extensive. A reference which would anticipate the invention of one group would not necessarily anticipate or make obvious any of the other groups. Furthermore, MPEP 803.04 sets forth that biological molecules with different sequences are separate inventions. A single sequence encoding a single polypeptide is a reasonable number based, upon the fact that each separate nucleic acid sequence encodes a distinct biological protein with a separate primary, secondary, and tertiary structure, as well as distinct biological activity and function. Clearly different searches and issues are involved in the examination of each Group. As such, search and examination of all the disparate unrelated proteins and nucleic acids of the claims would present a "serious burden".

The requirement is still deemed proper and is therefore made FINAL.

4. Claims 10-12, 14-21, 33, 48, 61 and 73 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in Paper No. 7.

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Claim Rejections - 35 U.S.C. § 112

5. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

7. Claims 22-32, 34-47, 49-60, 62-72 and 74-92 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a written description rejection.

The Guidelines for the Examination of Patent Applications Under the 35 U.S.C. 112, ¶ 1 "Written Description" Requirement make clear that the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice, reduction to drawings, or by disclosure of relevant, identifying characteristics, i.e., structure or other physical and or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the genus (Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001, see especially page 1106 3rd column).

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It is noted that SEQ ID NO:65 is a genomic DNA fragment. The specification does not disclose that SEQ ID NO:65 is drawn to a full length open reading frame. The claims reciting "comprising" and "encoding" language read upon complete gene sequences having in common a nucleotide sequence of SEQ ID NO:65 from any source. The claims also encompass polypeptide and polynucleotide variants, hybridizing variants and nucleic acid encoding epitopes. With the exception of SEQ ID NO:65, the skilled artisan cannot envision the detailed chemical structure of the encompassed polynucleotides, regardless of the simplicity of the method of isolation, absent further guidance. Since the claimed genus encompasses undisclosed genes, partial genomic sequences, and genes yet to be discovered, and variants thereof, the disclosed structural feature (i.e., the nucleic acid consisting of SEQ ID NO:65 encoding a polypeptide consisting of SEQ ID NO:66) does not constitute a substantial portion of the claimed genus. Absent a written description disclosing a representative number of nucleic acid sequences from this broad class of polynucleotides, the specification fails to show that applicant was "in possession of the claimed invention" at the time the application for patent was filed. In addition, claim 2 recites a nucleic acid comprising a nucleotide sequence comprising a sequence which specifically hybridizes to a nucleic acid comprising a sequence as set forth in SEQ ID NO:65 or variant thereof as part of the invention. However, there does not appear to be an adequate written description in the specification as-filed of the essential structural feature of the instantly recited nucleic acids, nor a correlation between a particular structure and function. The genus of nucleic acid probes which would hybridize to a nucleic acid comprising SEQ ID NO:65 is very large, encompassing not only sequences with polymorphisms and mutations compared to SEQ ID NO:65, but also sequences having no shared sequence with SEQ ID NO:65 itself since the hybridization could occur within the non-SEQ ID NO:65 portion of

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the nucleic acid comprising SEQ ID NO:65 or encoding SEQ ID NO:66. Further, no function is required of this hybridizing nucleic acid. Thus the genus of nucleic acids encompassed by this claim is extensive, and there does not appear to be any requirement that the nucleic acid probes share either a particular structure, a particular function, nor a correlation between some partial structure and a particular function. Consequently, SEQ ID NO:65 again does not appear to constitute a substantial portion of the claimed genus. Since these various nucleic acids do not possess defined structures, fragments of these nucleic acids also lack adequate written description, as do vectors, host cells, and associated methods using such. The genus of nucleic acids encompassed by the instant claims is much more extensive than SEQ ID NO:65 itself or internal fragments of SEQ ID NO:65 that could be used as probes or primers. The instant claim language opens up the claims to "flanking" sequences of undisclosed structure/sequence and unlimited length and variants within that structure that encode polypeptides or polynucleotides not disclosed in the specification. It is because of this open language that the specification fails to provide an adequate written description of the instant claims. However, the mere statement that a genus of nucleic acids is part of the invention and reference to a potential method for isolating some of these nucleic acids is not adequate written description of those nucleic acids. Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written description inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.). Adequate written description requires more than a mere statement that it is part of the invention and

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reference to a potential method for isolating it. The nucleic acid itself is required. See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993), and Amgen Inc. V. Chugai Pharmaceutical Co. Ltd., 18 USPQ2d 1016. Consequently, Applicant was not in possession of the instant claimed invention. Applicant is reminded that Vas-Cath makes clear that the written description provision of 35 U.S.C. 112 is severable from its enablement provision. (See page 1115.) Further, Reagents of the University of California v. Eli Lilly and Co. 43 USPQ2d 1398, appears to be directly relevant to the instant fact pattern. In Eli Lilly the specification and generic claims to all cDNAs encoding for vertebrate or mammalian insulin did not describe the claimed genus because they did not set forth any common features possessed by members of the genus that distinguished them from others. Id. at 1568, 43 USPQ2d at 1405. Nor did the specification describe a sufficient number of species within the very broad genus to indicate that the inventors had made a generic invention, *i.e.*, that they had possession of the breadth of the genus, as opposed to merely one or two such species. Id. In the instant case, Applicant has described a single species (the nucleic acid consisting of SEQ ID NO:65), but is attempting to claim an extremely broad genus of nucleic acids which do not necessarily share any common feature with SEQ ID NO:65.

8. Claims 22-32, 34-47, 49-60, 62-72 and 74-92 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated polynucleotide consisting of SEQ ID NO: 65, specific fragments thereof, vectors and host cells consisting of these, it does not reasonably provide enablement for an isolated polynucleotide comprising SEQ ID NO: 65 or a nucleic acid sequence encoding an amino acid sequence comprising SEQ ID NO:66 or epitope bearing portions thereof. The specification does not enable any person skilled in the art to which it pertains, or with

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which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

Applicant's specification (page 5, lines 17-37) sets forth that the polynucleotide of the invention can be used diagnostically. However, such a detection is limited to consisting of SEQ ID NO: 65 or specific fragments thereof, since the addition of an indefinite number of nucleotides 3' and 5' to SEQ ID NO:65 would unpredictably effect the ability to use SEQ ID NO:65 in a well established manner. Applicant's have not demonstrated that large sequences comprising SEQ ID NO:65 have this ability. Moreover, it is clear from a comparison of SEQ ID NO:65 with the art, that SEQ ID NO:65 encodes only a fragment of a larger protein. In the absence of the disclosure of a complete open reading frame, one skilled in the art would have reason to doubt that the protein of SEQ ID NO:66 is even produced by the bacterium. In the absence of the complete open reading frame, one of skill would have reason to doubt the production of the polypeptide by the bacterium and its asserted use as a diagnostic or use to make antibodies for diagnostic purposes. The specification fails to teach the activity or function of SEQ ID NO:66. The essential element of the claims are a bacterial polypeptide or bacterial antigen or epitope that is the full length open reading frame which is essential to the operation/function of the invention or the well established use as a bacterial antigen. The instant specification does not provide functional or structural characterization of the full length open reading frame of the instantly claimed bacterial polypeptide and polynucleotide which encodes the polypeptide. The specification does not provide a clear protocol by which the bacterial antigen comprising SEQ ID NO:66 was isolated from the microorganism of interest at the time the invention was made. The specification does not provide structural characterization of the complete open reading frame of the bacterial antigen (both start

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and stop codons). In the instant case, the classical start codon, methionine, is missing from the beginning of the bacterial polypeptide of SEQ ID NO:66. Absent characterization of the start codon, the genus of bacterial polynucleotides encoding proteins comprising SEQ ID NO:66 or fragments thereof is highly variant. One cannot enable that which one has not described. It is known for nucleic acids as well as proteins, for example, that even a single nucleotide or amino acid change or mutation can destroy the function of the biomolecule in many instances (e.g, hemoglobin of sickle cell anemia involves a single amino acid substitution of valine for glutamate), albeit not in all cases. The effects of these changes are largely unpredictable as to which ones have a significant effect versus not. Further, the specification fails to teach any function for the polypeptide such that one skilled in the art would be able to screen for functionally equivalent variants and no guidance is provided by the specification as to those substitutions that could be made. The specification and claims do not indicate what distinguishing attributes are shared by the members of the genus. Thus, the scope of the claims includes numerous structural variants, and the genus is highly variant because a significant number of structural differences between genus members is permitted. Since the disclosure fails to describe the common attributes or characteristics that identify members of the genus, and because the genus is highly variant, the DNA of SEQ ID NO:65, which encodes the protein fragment of SEQ ID NO:66, is insufficient to describe the genus of nucleic acids comprising SEQ ID NO:65, variants, epitopes and hybridizing nucleic acids. Thus, Applicant's have not described a function which would adequately describe the genus of nucleic acids or the genus of polypeptide. One of skill in the art would reasonably conclude that the disclosure as filed fails to provide a representative number of species to describe

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the genus. Thus, applicant is not enabled for the claimed genus and it would require undue experimentation to make an use such.

Therefore, only an isolated polynucleotide consisting of SEQ ID NO:65, consisting of particular fragments of SEQ ID NO:65, vectors and host cells, but not the full breadth of the claim is enabled by the instant specification.

9. Claims 65, 66, 68, 69, 71 and 72 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Applicant's claim language encompasses methods of producing proteins encoded by a strand complementary to the coding sequence or such polynucleotides further comprising heterologous sequences and wherein the heterologous sequences encode a heterologous polypeptide. One of skill in the art would be unable to practice such a claim. Complementary is routinely used in the art to describe the opposite (reverse complement) strand of a given DNA sequence (e.g., page 608, lines 5-6 of paragraph 1, Watson et al "Molecular Biology of the Gene" 4th Edition (1987) Benjamin-Cummings Publishing Company, Inc. USA), therefore the claims read upon a method of producing a polypeptide encoded by a sequence antisense to the coding strand. It is well known that antisense sequences do not encode products related to the sense strand, for example, the 5'-3' directionality is reversed, and therefore each codon triplet is read in the reverse orientation (encoding a different amino acid in most instances) and the N and C terminal of the encoded product is reversed. Applicant has not provided any guidance or working examples which would lead one of skill in the art to predict, first, that the antisense of SEQ ID NO:65 does, in fact, encode a protein product (e.g., start sequences, methionine codon, a substantial open

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reading frame, stop and other termination signals). Further one of skill in the art would not predict such a product would be structurally or functionally related, and Applicant has not provided any potential means of using such an unrelated protein.

In view of the lack of guidance, lack of working examples, one of skill in the art would be forced into undue experimentation to practice the claimed invention.

10. Claims 41 and 86-92 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

As to claim 41, the claim improperly depends from itself and therefore is prima facie indefinite. It appears that claim 41, should properly depend from claim 40.

As to claims 86 and dependent claims 87-92, the claims are indefinite from the recitation of "...consisting of at least 100 contiguous nucleotides..". The term "consisting of" is closed language, however "at least" appears to indicate that the polynucleotide can be larger. Therefore, the combination of "consisting of" and "at least" presents a fundamental contradiction that renders the metes and bounds of the claimed subject polynucleotide indefinite.

Claim Rejections - 35 U.S.C. § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless --

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

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(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language

11. Claim 62 is rejected under 35 U.S.C. 102(b) as being anticipated by Birkett et al (U.S. Patent Number 5,302,527) or Boehringer Mannheim 1991 Catalog or Stratagene 1991 Product Catalog.

The claim is drawn to an isolated polynucleotide comprising a nucleic acid sequence which hybridizes under stringent conditions to SEQ ID NO:65, encoding variant or 95% identical variant or the complementary strand.

Birkett et al (U.S. Patent Number 5,302,527) disclose of random priming with a mixed hexamer oligonucleotide kit (Multiprime Kit, Amersham). (See column 15 lines 25-30). In view that the random hexamer oligonucleotides comprise every possible combination of six consecutive nucleotides and that these sequences will inherently hybridize to the recited sequences under the recited conditions, the disclosure of the hexamer kit by Birkett et al is seen to anticipate the claimed invention.

Boehringer Mannheim Biochemicals teach isolated random primers (6-mers) for random priming of DNA. These sequences will inherently hybridize to the recited sequences under the recited conditions.

Stratagene 1991 product catalog teaches random 9-mer primers for random priming of DNA. These sequences will inherently hybridize to the recited sequences under the recited conditions.

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12. Claims 34, 49, 62, 65, 66, 67, 68, 69, 70, 71 are 86-92 are rejected under 35 U.S.C. 102(e) as being anticipated by Bergeron et al (U.S. Patent No. 6,001,564 issued December 14, 1999, filed September 11, 1995).

Bergeron et al teach SEQ ID NO:34 which is a genomic DNA fragment.

Bergeron et al disclose SEQ ID NO:34 as a double stranded nucleic acid sequence (see column 89). SEQ ID NO:34 comprises 106 consecutive nucleotides in common with SEQ ID NO:65 (see attached alignment). Bergeron et al teach fragment of at least twelve but not less than 100 nucleotides in length are useful for probes for the detection of bacteria (see column 4, lines 9-14 and column 6, lines 62-65). The double stranded nucleic acid encodes a protein having 29 consecutive amino acids in common with SEQ ID NO:66 (see attached alignment). The isolated genomic fragments were generated by digesting genomic DNA with SauA1 and ligated into the bacterial plasmid vector pGEM3Zf (Promega). The recombinant plasmids were then used to transform a competent E. coli DH5 α to form a genomic library. Therefore, the isolated genomic nucleic acid sequence represented by SEQ ID NO:34 is taught in a vector (i.e. heterologous nucleic acid sequence, operably linked promoter are inherent features of the Promega pGEM3Zf plasmid) and in a host cell. As such, Bergeron et al anticipates the claimed nucleic acids, vectors, host cells and methods of making such.

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Citation of Relevant Art

13. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

Promega Protocols and Applications Guide Second edition, 1991, pages 45-74 is cited to teach the pGEM plasmid vectors and specifically the pGEM3Z plasmids (see at least page 47 paragraph bridging columns 1-2).

Status of Claims

14. No claims are allowed.

15. Any inquiry of a general nature or relating to the status of this general application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Papers relating to this application may be submitted to Technology Center 1600, Group 1640 by facsimile transmission. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). Should applicant wish to FAX a response, the current FAX number for Group 1600 is (703) 308-4242.

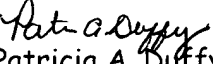
Any inquiry concerning this communication or earlier communications from the examiner should be directed to Patricia A. Duffy, Ph.D. whose telephone number is (703) 305-7555. The examiner can normally be reached on Monday-Friday from 9:30 AM to 6:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith, can be reached at (703) 308-3909.

Patricia A. Duffy, Ph.D.
May 2, 2003

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Patricia A. Duffy, Ph.D.
Primary Examiner
Group 1600

RESULT 20
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 LOC 841 bp DN linear PAT 08-SEP-2000
 DEFINITION Sequence 34 from patent US 6001564.
 ACCESSION AR093475
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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 RENCE 1 (bases 1 to 841)
 THORS Bergeron, M.G., Ouellette, M. and Roy, P.H.
 TLE Species specific and universal DNA probes and amplification primers
 to rapidly detect and identify common bacterial pathogens and
 associated antibiotic resistance genes from clinical specimens for
 routine diagnosis in microbiology laboratories
 JRNAL Patent: US 6001564-A 34 14-DEC-1999;
 JRES Location/Qualifiers
 source 1..841
 /organism="unknown"
 COUNT 205 a 163 c 142 g 331 t
 IN

Query Match 6.4%; Score 146; DB 6; Length 841;
 Percent Local Similarity 99.5%; Pred. No. 1.1e-69;
 Mismatches 196; Conservative 0; Indels 1; Gaps 0;
 2001 CGCATTGAGATAATGGTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTC 2060
 Db 797 CGCATTGAGATAATGGTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTC 738
 QY 2061 AAGCTGATACCAATCAAACGGAACCAACGAGGAGAAACCTCAGACAGAAAAACCTG 2120
 Db 737 AAGCTGATACCAATCAAACGGAACCAACGAGGAGAAACCTCAGACAGAAAAACCTG 678
 QY 2121 AGGAAGAAACCCCTCGAGAAGAGAAACCGCAAAGCGAGAAACAGAGTCTCCAAACCAA 2180
 Db 677 AGGAAGAAACCCCTCGAGAAGAGAAACCGCAAAGCGAGAAACAGAGTCTCCAAACCAA 618
 QY 2181 CAGAGGAACCAAGAA 2197
 Db 617 CAGAGGAACCAAGAA 601

29
 60
 17
 106

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 APPLICATION NUMBER: US 08/304,732
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 ATTORNEY/AGENT INFORMATION:
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 REFERENCE/DOCKET NUMBER: 850586.90012
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 TELEPHONE: (414) 277-5000
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 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 841 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus pneumoniae
 US-08-526-840B-34

Alignment Scores:
 Pred. No.: 9.83e-40 Length: 841
 Score: 512.00 Matches: 104
 Percent Similarity: 93.10% Conservative: 4
 Best Local Similarity: 89.66% Mismatches: 2
 Query Match: 12.74% Indels: 7
 DB: 3 Gaps: 2

US-09-765-272A-66 (1-763) x US-08-526-840B-34 (1-841)

QY 653 LeuAlaThrValLysTyrTyrValGluHisProAsnGluArgProHisSerAspAsnGly 672
 Db 839 TTGGCGACTGTCAAGTACTATGTGCAACATCCAAACGAACGTCGATTTCAGATAATGGT 781
 QY 673 PheGlyAsnAlaSerAspHisValGlnArgAsnLysAsnGlyGlnAlaAspThrAsnGln 692
 Db 780 TTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTCAAGCTGATACCAATCAA 721
 QY 693 ThrGluLysProSerGluGluLysProGlnThrGluLysProGluGluGluThrProArg 712
 Db 720 ACGGAAAAACCAACGAGGAGAAACCTCAGACAGAAAAACCTGAGGAAGAAACCCCTCGA 661
 QY 713 GluGluLysProGlnSerGluLysProGluSerProLysProThrGluGlu----- 729
 Db 660 GAAGAGAAACCGCAAAGCGAGAAACAGAGTCTCCAAACCAACAGAGGAACCAAGAA 601

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